

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (currently amended): A method of normalizing gene expression data, the method comprising the steps of:

i) indicating data x and y concerning expression quantities, which have been obtained for a first sample and a second sample, respectively, with points plotted on a logarithmic coordinate system, in which a horizontal axis represents logarithms of the expression quantities obtained for the first sample, and in which a vertical axis represents logarithms of the expression quantities obtained for the second sample,

ii) calculating a coefficient 10^{-a} from a value of an intercept "a" of an approximate straight line, which is obtained from approximate representation of the plotted points with a straight line having a slope of 1, on the vertical axis, and wherein x, y and "a" form a relationship $\log y = \log x + a$;

iii) performing division processing for dividing the data concerning the expression quantities for the second sample, by the coefficient, whereby the data concerning the expression quantities having been obtained for the second sample are normalized as y' where $y' = y/10^a$ and

iv) outputting a result y' of step iii.

2. (original): A method as defined in Claim 1 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.

3 - 4. (canceled)

5. (currently amended): A method of normalizing gene expression data, the method comprising the steps of:

i) plotting a logarithmic graph of data x and y related to a first sample versus data related to a second sample, respectively the data related to the second sample being on a vertical axis;

ii) calculating a coefficient 10^a from an intercept "a" formed by a straight line with a slope of 1 with a vertical axis, the straight line approximating the plotted points wherein x, y and "a" form a relationship $\log y = \log x + a$; and

iii) dividing the data related to the second sample by the coefficient 10^a to normalize the data for the second sample as y' where $y' = y/10^a$ and

iv) outputting a result of y' of step iii.

6. (currently amended): A method as defined in Claim [[4]] 5 wherein the first sample is a sample obtained from a normal cell, and the second sample is a sample obtained from an abnormal cell.